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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/988,462

DATE: 01/08/2002
 TIME: 15:38:44

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ENTERED

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: Koziel, Michael G.
 7 Desai, Nalini M.
 8 Lewis, Kelly S.
 9 Kramer, Vance C.
 10 Warren, Gregory W.
 11 Evola, Stephen V.
 12 Crossland, Lyle D.
 13 Wright, Martha S.
 14 Merlin, Ellis J.
 15 Launis, Karen L.
 W--> 16 Rothstein, Steven J.
 W--> 17 Bowman, Cindy G.
 W--> 18 Dawson, John L.
 W--> 19 Dunder, Erik M.
 W--> 20 Pace, Gary M.
 W--> 21 Suttie, Janet L.

23 (ii) TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
 24 INSECTICIDAL ACTIVITY IN MAIZE

26 (iii) NUMBER OF SEQUENCES: 94

28 (iv) CORRESPONDENCE ADDRESS:
 29 (A) ADDRESSEE: Syngenta Biotechnology, Inc.
 30 (B) STREET: 3054 Cornwallis Road
 31 (C) CITY: Research Triangle Park
 32 (D) STATE: NC
 33 (E) COUNTRY: USA
 34 (F) ZIP: 27709

36 (v) COMPUTER READABLE FORM:
 37 (A) MEDIUM TYPE: Floppy disk
 38 (B) COMPUTER: IBM PC compatible
 39 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 40 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

42 (vi) CURRENT APPLICATION DATA:
 C--> 43 (A) APPLICATION NUMBER: US/09/988,462
 C--> 44 (B) FILING DATE: 20-Nov-2001
 45 (C) CLASSIFICATION:

59 (vii) PRIOR APPLICATION DATA:
 48 (A) APPLICATION NUMBER: US 09/547,422
 49 (B) FILING DATE: 11-APR-2000
 52 (A) APPLICATION NUMBER: US 08/459,504
 53 (B) FILING DATE: 02-JUN-1995
 56 (A) APPLICATION NUMBER: US 07/951,715
 57 (B) FILING DATE: 25-SEP-1992
 60 (A) APPLICATION NUMBER: US 07/772,027
 61 (B) FILING DATE: 04-OCT-1991

63 (viii) ATTORNEY/AGENT INFORMATION:

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64      (A) NAME: Meigs, J. Timothy
65      (B) REGISTRATION NUMBER: 38,241
66      (C) REFERENCE/DOCKET NUMBER: S-18805I
68      (ix) TELECOMMUNICATION INFORMATION:
69          (A) TELEPHONE: (919)541-8587
70          (B) TELEFAX: (919)541-8689
72 (2) INFORMATION FOR SEQ ID NO: 1:
73      (i) SEQUENCE CHARACTERISTICS:
74          (A) LENGTH: 3468 base pairs
75          (B) TYPE: nucleic acid
76          (C) STRANDEDNESS: single
77          (D) TOPOLOGY: linear
80      (ii) MOLECULE TYPE: DNA (genomic)
82      (iii) HYPOTHETICAL: NO
84      (vi) ORIGINAL SOURCE:
85          (A) ORGANISM: Bacillus thuringiensis kurstaki
86          (B) STRAIN: HD-1
88      (ix) FEATURE:
89          (A) NAME/KEY: misc_feature
90          (B) LOCATION: 1..3468
91          (D) OTHER INFORMATION: /product= "Full-length native
92 cryIA(b)"
93 /note= "Appears in Figures 1 and 4 as BTHKURHD."
96      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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100 GTAGAAGTAT TAGGTGGAGA AAGAATAGAA ACTGGTTACA CCCCAATCGA TATTCCTTG      120
102 TCGCTAACGC AATTTCTTTT GAGTGAATTT GTTCCCGGTG CTGGATTTGT GTTAGGACTA      180
104 GTTGATATAA TATGGGGAAT TTTTGGTCCC TCTCAATGGG ACGCATTTCT TGTACAAATT      240
106 GAACAGTTAA TTAACCAAAG AATAGAAGAA TTCGCTAGGA ACCAAGCCAT TTCTAGATTA      300
108 GAAGGACTAA GCAATCTTTA TCAAATTTAC GCAGAATCTT TTAGAGAGTG GGAAGCAGAT      360
110 CCTACTAATC CAGCATTAAG AGAAGAGATG CGTATTCAAT TCAATGACAT GAACAGTGCC      420
112 CTTACAACCG CTATTCCTCT TTTTGCAGTT CAAAATTATC AAGTTCCTCT TTTATCAGTA      480
114 TATGTTCAAG CTGCAAATTT ACATTTATCA GTTTTGAGAG ATGTTTCAGT GTTTGGACAA      540
116 AGGTGGGGAT TTGATGCCGC GACTATCAAT AGTCGTTATA ATGATTTAAC TAGGCTTATT      600
118 GGCAACTATA CAGATCATGC TGTACGCTGG TACAATACGG GATTAGAGCG TGTATGGGGA      660
120 CCGGATTCTA GAGATTGGAT AAGATATAAT CAATTTAGAA GAGAATTAAC ACTAAGTGT      720
122 TTAGATATCG TTTCTCTATT TCCGAATAT GATAGTAGAA CGTATCCAAT TCGAACAGTT      780
124 TCCCAATTAA CAAGAGAAAT TTATACAAAC CCAGTATTAG AAAATTTTGA TGGTAGTTTT      840
126 CGAGGCTCGG CTCAGGCGAT AGAAGGAAGT ATTAGGAGTC CACATTTGAT GGATATACTT      900
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130 ATAATGGCTT CTCCTGTAGG GTTTTCGGGG CCAGAATTCA CTTTCCGCT ATATGGAAC      1020
132 ATGGGAAATG CAGCTCCACA ACAACGTATT GTTGCTCAAC TAGGTCAGGG CGTGATAGA      1080
134 ACATTATCGT CCACCTTTATA TAGAAGACCT TTTAATATAG GGATAAATA TCAACAAC      1140
136 TCTGTTCTTG ACGGGACAGA ATTTGCTTAT GGAACCTCCT CAAATTTGCC ATCCGCTGTA      1200
138 TACAGAAAAA GCGGAACGGT AGATTCGCTG GATGAAATAC CGCCACAGAA TAACAACGTG      1260
140 CCACCTAGGC AAGGATTTAG TCATCGATTA AGCCATGTTT CAATGTTTCG TTCAGGCTTT      1320
142 AGTAATAGTA GTGTAAGTAT AATAAGAGCT CCTATGTTCT CTTGGATACA TCGTAGTGCT      1380
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154 TTACAGTCCG GAAGCTTTAG GACTGTAGGT TTTACTACTC CGTTTAACTT TTCAAATGGA 1740
156 TCAAGTGTAT TTACGTTAAG TGCTCATGTC TTCAATTGAG GCAATGAAGT TTATATAGAT 1800
158 CGAATTGAAT TTGTTCCGGC AGAAGTAACC TTTGAGGCAG AATATGATTT AGAAAGAGCA 1860
160 CAAAAGGCGG TGAATGAGCT GTTTACTTCT TCCAATCAAA TCGGGTTAAA AACAGATGTG 1920
162 ACGGATTATC ATATTGATCA AGTATCCAAT TTAGTTGAGT GTTTATCTGA TGAATTTTGT 1980
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166 CGGAATTTAC TTCAAGATCC AAACCTTTAGA GGGATCAATA GACAAC TAGA CCGTGGCTGG 2100
168 AGAGGAAGTA CGGATATTAC CATCCAAGGA GGCGATGACG TATTCAAAGA GAATTACGTT 2160
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174 TTAGAAATCT ATTTAATTCG CTACAATGCC AAACACGAAA CAGTAAATGT GCCAGGTACG 2340
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178 CATTTCTCCT TGGACATTGA TGTTGGATGT ACAGACTTAA ATGAGGACTT AGGTGTATGG 2460
180 GTGATATTCA AGATTAAGAC GCAAGATGGC CATGCAAGAC TAGGAAATCT AGAATTTCTC 2520
182 GAAGAGAAAC CATTAGTAGG AGAAGCACTA GCTCGTGTGA AAAGAGCGGA GAAAAAATGG 2580
184 AGAGACAAAC GTGAAAAATT GGAATGGGAA ACAAATATTG TTTATAAAGA GGCAAAAGAA 2640
186 TCTGTAGATG CTTTATTTGT AAACCTCTCA TATGATAGAT TACAAGCGGA TACCAACATC 2700
188 GCGATGATTC ATGCGGCAGA TAAACGCGGT CATAGCATTG GAGAAGCTTA TCTGCCTGAG 2760
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192 ACTGCATTCT CCCTATATGA TGCGAGAAAT GTCATTAAAA ATGGTGATTT TAATAATGGC 2880
194 TTATCCTGCT GGAACGTGAA AGGGCATGTA GATGTAGAAG AACAAAACAA CCACCGTTTCG 2940
196 GTCCTTGTG TTCCGGAATG GGAAGCAGAA GTGTCACAAG AAGTTCGTGT CTGTCCGGGT 3000
198 CGTGGCTATA TCCTTCGTGT CACAGCGTAC AAGGAGGGAT ATGGAGAAGG TTGCGTAACC 3060
200 ATTATGAGA TCGAGAACAA TACAGACGAA CTGAAGTTTA GCAACTGTGT AGAAGAGGAA 3120
202 GTATATCCAA ACAACACGGT AACGTGTAAT GATTATACTG CGACTCAAGA AGAATATGAG 3180
204 GGTACGTACA CTTCTCGTAA TCGAGGATAT GACGGAGCCT ATGAAAGCAA TTCTTCTGTA 3240
206 CCAGCTGATT ATGCATCAGC CTATGAAGAA AAAGCATATA CAGATGGACG AAGAGACAAT 3300
208 CCTTGTGAAT CTAACAGAGG ATATGGGGAT TACACACCAC TACCAGCTGG CTATGTGACA 3360
210 AAAGAATTAG AGTACTTCCC AGAAACCGAT AAGGTATGGA TTGAGATCGG AGAAACGGAA 3420
212 GGAACATTCA TCGTGGACAG CGTGGAATTA CTTCTTATGG AGGAATAA 3468

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214 (2) INFORMATION FOR SEQ ID NO: 2:

216 (i) SEQUENCE CHARACTERISTICS:

217 (A) LENGTH: 3468 base pairs

218 (B) TYPE: nucleic acid

219 (C) STRANDEDNESS: single

220 (D) TOPOLOGY: linear

222 (ii) MOLECULE TYPE: other nucleic acid

223 (A) DESCRIPTION: /desc = "Synthetic DNA"

225 (iii) HYPOTHETICAL: NO

228 (ix) FEATURE:

229 (A) NAME/KEY: misc_feature

230 (B) LOCATION: 1..3468

231 (D) OTHER INFORMATION: /product= "Full-length pure maize

232 optimized synthetic Bt"

233 /note= "Disclosed in Figure 3 as syn1T.mze"

236 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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242	AGCCTGACCC	AGTTCCTGCT	GAGCGAGTTC	GTGCCCCGCG	CCGGCTTCGT	GCTGGGCCTG	180
244	GTGGACATCA	TCTGGGGCAT	CTTCGGCCCC	AGCCAGTGGG	ACGCCTTCCT	GGTGCAGATC	240
246	GAGCAGCTGA	TCAACCAGCG	CATCGAGGAG	TTCGCCCCGA	ACCAGGCCAT	CAGCCGCCTG	300
248	GAGGGCCTGA	GCAACCTGTA	CCAGATCTAC	GCCGAGAGCT	TCCGCGAGTG	GGAGGCCGAC	360
250	CCCACCAACC	CCGCCCTGCG	CGAGGAGATG	CGCATCCAGT	TCAACGACAT	GAACAGCGCC	420
252	CTGACCACCG	CCATCCCCCT	GTTCGCCGTG	CAGAACTACC	AGGTGCCCCCT	GCTGAGCGTG	480
254	TACGTGCAGG	CCGCCAACCT	GCACCTGAGC	GTGCTGCGCG	ACGTGAGCGT	GTTCCGGCCAG	540
256	CGCTGGGGCT	TCGACGCCGC	CACCATCAAC	AGCCGCTACA	ACGACCTGAC	CCGCCTGATC	600
258	GGCAACTACA	CCGACCACGC	CGTGCCTGG	TACAACACCG	GCCTGGAGCG	CGTGTGGGGC	660
260	CCCACAGCC	GCGACTGGAT	CCGCTACAAC	CAGTTCGCC	GCGAGCTGAC	CCTGACCGTG	720
262	CTGGACATCG	TGAGCCTGTT	CCCCAACTAC	GACAGCCGCA	CCTACCCCAT	CCGCACCGTG	780
264	AGCCAGCTGA	CCCGCGAGAT	CTACACCAAC	CCCGTGCTGG	AGAACTTCGA	CGGCAGCTTC	840
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274	ACCCTGAGCA	GCACCCTGTA	CCGCCGCCCC	TTCAACATCG	GCATCAACAA	CCAGCAGCTG	1140
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278	TACCGCAAGA	GCGGCACCGT	GGACAGCCTG	GACGAGATCC	CCCCCAGAA	CAACAACGTG	1260
280	CCCCCCCCGCC	AGGGCTTCAG	CCACCGCCTG	AGCCACGTGA	GCATGTTCCG	CAGCGGCTTC	1320
282	AGCAACAGCA	GCGTGAGCAT	CATCCGCGCC	CCCATGTTCA	GCTGGATCCA	CCGCAGCGCC	1380
284	GAGTTCAACA	ACATCATCCC	CAGCAGCCAG	ATCACCCAGA	TCCCCCTGAC	CAAGAGCACC	1440
286	AACCTGGGCA	GCGGCACCAG	CGTGGTGAAG	GGCCCCGGCT	TCACCGGCGG	CGACATCCTG	1500
288	CGCCGCACCA	GCCCCGGCCA	GATCAGCACC	CTGCGCGTGA	ACATCACCGC	CCCCCTGAGC	1560
290	CAGCGCTACC	GCGTGCGCAT	CCGCTACGCC	AGCACCAACA	ACCTGCAGTT	CCACACCAGC	1620
292	ATCGACGGCC	GCCCCATCAA	CCAGGGCAAC	TTCAGCGCCA	CCATGAGCAG	CGGCAGCAAC	1680
294	CTGCAGAGCG	GCAGCTTCCG	CACCGTGCGC	TTCAACACCC	CCTTCAACTT	CAGCAACGGC	1740
296	AGCAGCGTGT	TCACCCTGAG	CGCCCACGTG	TTCAACACCG	GCAACGAGGT	GTACATCGAC	1800
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302	ACCGACTACC	ACATCGACCA	GGTGAGCAAC	CTGGTGAGT	GCCTGAGCGA	CGAGTTCTGC	1980
304	CTGGACGAGA	AGAAGGAGCT	GAGCGAGAAG	GTGAAGCACG	CCAAGCGCCT	GAGCGACGAG	2040
306	CGCAACCTGC	TGCAGGACCC	CAACTTCCGC	GGCATCAACC	GCCAGCTGGA	CCGCGGCTGG	2100
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310	ACCCTGCTGG	GCACCTTCGA	CGAGTGCTAC	CCCACCTACC	TGTACCAGAA	GATCGACGAG	2220
312	AGCAAGCTGA	AGGCCTACAC	CCGCTACCAG	CTGCGCGGCT	ACATCGAGGA	CAGCCAGGAC	2280
314	CTGGAGATCT	ACCTGATCCG	CTACAACGCC	AAGCACGAGA	CCGTGAACGT	GCCCCGCCAC	2340
316	GGCAGCCTGT	GGCCCCTGAG	CGCCCCCAGC	CCCATCGGCA	AGTGCGCCCA	CCACAGCCAC	2400
318	CACTTCAGCC	TGGACATCGA	CGTGGGCTGC	ACCGACCTGA	ACGAGGACCT	GGGCGTGTGG	2460
320	GTGATCTTCA	AGATCAAGAC	CCAGGACGGC	CACGCCCCGC	TGGGCAACCT	GGAGTTCCTG	2520
322	GAGGAGAAGC	CCCTGGTGGG	CGAGGCCCTG	GCCCCGCTGA	AGCGCGCCGA	GAAGAAGTGG	2580
324	CGCGACAAGC	GCGAGAAGCT	GGAGTGGGAG	ACCAACATCG	TGTACAAGGA	GGCCAAGGAG	2640
326	AGCGTGAGCG	CCCTGTTCTG	GAACAGCCAG	TACGACCGCC	TGCAGGCCGA	CACCAACATC	2700
328	GCCATGATCC	ACGCCGCCGA	CAAGCGCGTG	CACAGCATCC	GCGAGGCCTA	CCTGCCCGAG	2760
330	CTGAGCGTGA	TCCCCGGCGT	GAACGCCGCC	ATCTTCGAGG	AGCTGGAGGG	CCGCATCTTC	2820
332	ACCGCCTTCA	GCCTGTACGA	CGCCCCGAAC	GTGATCAAGA	ACGGCGACTT	CAACAACGGC	2880
334	CTGAGCTGCT	GGAACGTGAA	GGGCCACGTG	GACGTGGAGG	AGCAGAACAA	CCACCGCAGC	2940

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340 ATCCACGAGA TCGAGAACAA CACCGACGAG CTGAAGTTCA GCAACTGCGT GGAGGAGGAG 3120
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344 GGCACCTACA CCAGCCGCAA CCGCGGCTAC GACGGCGCCT ACGAGAGCAA CAGCAGCGTG 3240
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348 CCCTGCGAGA GCAACCGCGG CTACGGCGAC TACACCCCC TGCCCGCCGG CTACGTGACC 3360
350 AAGGAGCTGG AGTACTTCCC CGAGACCGAC AAGGTGTGGA TCGAGATCGG CGAGACCGAG 3420
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354 (2) INFORMATION FOR SEQ ID NO: 3:
356 (i) SEQUENCE CHARACTERISTICS:
357 (A) LENGTH: 1947 base pairs
358 (B) TYPE: nucleic acid
359 (C) STRANDEDNESS: single
360 (D) TOPOLOGY: linear
362 (ii) MOLECULE TYPE: other nucleic acid
363 (A) DESCRIPTION: /desc = "Synthetic DNA"
365 (iii) HYPOTHETICAL: NO
368 (ix) FEATURE:
369 (A) NAME/KEY: misc_feature
370 (B) LOCATION: 1..1947
371 (D) OTHER INFORMATION: /product= "Truncated synthetic
372 maize optimized cryIA(b) gene"
373 /note= "Disclosed in Figures 1, 2, 3, 4 and 5 as bssyn."
376 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
378 ATGGACAACA ACCCAACAT CAACGAGTGC ATCCCCTACA ACTGCCTGAG CAACCCCGAG 60
380 GTGGAGGTGC TGGGCGGCGA GCGCATCGAG ACCGGCTACA CCCCATCGA CATCAGCCTG 120
382 AGCCTGACCC AGTTCCTGCT GAGCGAGTTC GTGCCCGGCG CCGGCTTCGT GCTGGGCCTG 180
384 GTGGACATCA TCTGGGGCAT CTTCGGCCCC AGCCAGTGGG ACGCCTTCCT GGTGCAGATC 240
386 GAGCAGCTGA TCAACCAGCG CATCGAGGAG TTCGCCCCGA ACCAGGCCAT CAGCCGCCTG 300
388 GAGGGCCTGA GCAACCTGTA CCAAATCTAC GCCGAGAGCT TCCGCGAGTG GGAGGCCGAC 360
390 CCCACCAACC CCGCCCTGCG CGAGGAGATG CGCATCCAGT TCAACGACAT GAACAGCGCC 420
392 CTGACCACCG CCATCCCCCT GTTCGCCGTG CAGAACTACC AGGTGCCCCT GCTGAGCGTG 480
394 TACGTGCAGG CCGCCAACCT GCACCTGAGC GTGCTGCGCG ACGTCAGCGT GTTCGGCCAG 540
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398 GGCAACTACA CCGACCACGC CGTGCGCTGG TACAACACCG GCCTGGAGCG CGTGTGGGGT 660
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402 CTGGACATCG TGAGCCTGTT CCCCAACTAC GACAGCCGCA CCTACCCCAT CCGCACCGTG 780
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406 CGCGGCAGCG CCCAGGGCAT CGAGGGCAGC ATCCGCAGCC CCCACCTGAT GGACATCCTG 900
408 AACAGCATCA CCATCTACAC CGACGCCCAC CGCGCGAGT ACTACTGGAG CGGCCACCAG 960
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416 AGCGTGCTGG ACGGCACCGA GTTCGCCTAC GGCACCAGCA GCAACCTGCC CAGCGCCGTG 1200
418 TACCGCAAGA GCGGCACCGT GGACAGCCTG GACGAGATCC CCCCTCAGAA CAACAACGTG 1260
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422 AGCAACAGCA GCGTGAGCAT CATCCGTGCA CCTATGTTCA GCTGGATTCA CCGCAGTGCC 1380
424 GAGTTCAACA ACATCATCCC CAGCAGCCAA ATCACCAGA TCCCCCTGAC CAAGAGCACC 1440

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VERIFICATION SUMMARY

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L:44 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
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L:1337 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:8
L:1341 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:8
L:1345 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:8
L:1349 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:8
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L:1405 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:8
L:1409 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:8
L:1413 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:8
L:1417 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:8
L:1421 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:8

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/988,462

DATE: 01/08/2002

TIME: 15:38:46

Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF3\01082002\I988462.raw

L:1425 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:8
L:1429 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:8
L:1433 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:8
L:1437 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:8
L:1441 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:8
L:1445 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:8
L:1449 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:8
L:1453 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:8
L:1457 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:8
L:1461 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:8